EXHIBIT B:

MULTISPECIES COMPARISON OF STRAD POLYPEPTIDE

BLAST

Basic Local Alignment Search Tool

- •

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

STRAD comparison

Results for:

| ref|NP_001003787.1 STE20-related kinase adapter protein alpha isoform 1 [Homo sapiens] >gi|74759034|sp|Q7RTN6.1|STRAA_...(431aa) ▼ |

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
gi|51242955|ref|NP_001003787.1|
gi|51242955|ref|NP_001003787.1|
Description
STE20-related kinase adapter protein alpha isoform 1 [Homo sapiens] >gi|74759034|sp|Q7RTN6.1|STRAA_HUMAN RecName:
Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein; AltName:
Full=Serologically defined breast cancer antigen NY-BR-96 >gi|34494889|tpg|DAA01797.1| TPA_exp: STE20-related adaptor protein
[Homo sapiens] >gi|119614691|gb|EAW94285.1| protein kinase LYK5, isoform CRA_c [Homo sapiens]
Molecule type
amino acid
Query Length
431

Subject ID
4 subjects
Description
Molecule type
amino acid
Subject Length
n/a
Program
BLASTP 2.2.24+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Reference - compositional score matrix adjustment
Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005)
"Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.
Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]
Search Parameters

Search parameter name Search parameter value

Search parameter name	Search parameter value
Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

Params Ungapped Gapped

Params	Ungapped	Gapped
Lambda	0.318619	0.267
K	0.13404	0.041
H	0.398234	0.14

Results Statistics

Results Statistics parameter name Results Statistics parameter value

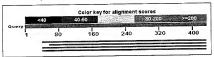| Results Statistics parameter name	Results Statistics parameter value
Effective search space	144800

Graphic Summary

Distribution of 4 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Descriptions

Legend for links to other resources: 🅄 UniGene 🄴 GEO 🄶 Gene 🅂 Structure 🄼 Map Viewer 🅟 PubChem BioAssay

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
XP_850260.1	PREDICTED: similar to protein kinase LYK5 isoform 2 isoform 1 [Canis familiaris]	786	786	90%	0.0	🅄🄶🄼
NP_001015603.1	STE20-related kinase adapter protein alpha [Bos taurus] >gi|240849233|ref|NP_001155356.1| STE20-related kinase adapter protein alpha [Ovis aries] >gi|75070042|sp|Q5E9J9.1|STRAA_BOVIN RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein >gi|59858207|gb|AAX08938.1| protein kinase LYK5 isoform 4 [Bos taurus] >gi|82856693|gb|ACR46653.1| STRADA [Ovis aries] >gi|296476245|gb|DAA18360.1| STE20-related kinase adapter protein alpha [Bos taurus] >ref|NP_001155356.1| STE20-related kinase adapter protein alpha [Ovis aries] >sp|Q5E9J9.1|STRAA_BOVIN RecName: Full=STE20-related adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein >gb|AAX08938.1| protein kinase LYK5 [Bos taurus] >gb|ACR46653.1| STRADA [Ovis aries] >gb|DAA18360.1| STE20-related kinase adapter protein alpha [Bos taurus]	748	748	86%	0.0	🅄🄶🄼
NP_082402.1	STE20-related kinase adapter protein alpha [Mus musculus] >gi|12847582|dbj|BAB27626.1| unnamed protein product [Mus musculus] >gi|33638094|gb|AAQ24157.1| protein kinase LYK5 splice variant 1 [Mus musculus] >gi|35192946|gb|AAH58517.1| RIKEN cDNA 2610019A05 gene [Mus musculus] >gi|17616946|gb|ABK42491.1| STLK5 [synthetic construct] >gi|123243203|amb|CAM27017.1| novel protein [Mus musculus] >gi|148702325|gb|EDL34272.1| RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus] >gi|148702326|gb|EDL34273.1| RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus] >dbj|BAB27628.1| unnamed protein product [Mus musculus] >gb|AAQ24157.1| protein kinase LYK5 splice variant 1 [Mus musculus] >gb|AAH58517.1| RIKEN cDNA 2610019A05 gene [Mus musculus] >gb|ABK42491.1| STLK5 [synthetic construct] >emb|CAM27017.1| novel protein [Mus musculus] >gb|EDL34272.1| RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus] >gb|EDL34273.1| RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus]	775	775	90%	0.0	🅄🄶🄼
NP_877972.1	STE20-related kinase adapter protein alpha [Rattus norvegicus] >gi|61912054|sp|Q7TNZ6.1|STRAA_RAT RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein >gi|33087213|gb|AAP92801.1| protein kinase LYK5 [Rattus norvegicus] >sp|Q7TNZ8.1|STRAA_RAT RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD alpha; AltName: Full=STE20-related adapter protein >gb|AAP92801.1| protein kinase LYK5 [Rattus norvegicus]	758	758	90%	0.0	🅄🄶🄼

Alignments

Select All Get selected sequences Distance tree of results Multiple alignment

```
>ref|XP_850260.1| 🅄🄶🄼 PREDICTED: similar to protein kinase LYK5 isoform 2 isoform 1
[Canis familiaris]
Length=394

GENE ID: 609377 STRADA | STE20-related kinase adaptor alpha
[Canis lupus familiaris]

Score = 786 bits (2030), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 376/390 (97%), Positives = 381/390 (98%), Gaps = 0/390 (0%)

Query  42   TNDASSESIASFSKQEVMSSFLPEGGCYELLTVIGKGFEDIMTVNLARYKFTGEYVTVRR  101
            TN+ASSESIAS SKQE+MSSFLPEGG YELLT+IGKGFEDIMTVNLARYKFTGEYVTVRR
Sbjct  5    TNEASSESIAS SKQE+MSSFLPEGG YELLT+IGKGFEDIMTVNLARYKFTGEYVTVRR  64

Query  102  INLEACSNEMVTFLQGELHVSKLFNHPNIVPYRATFIADNELWVVTSFMAYGSAXDLICT  161
            INLEACSNEMVTFLQGELHVSKLF+HPNI+PYRATFIADNELWVVTSFMAYGSAXDLICT
Sbjct  65   INLEACSNEMVTFLQGELHVSKLFNHPNI+PYRATFIADNELWVVTSFMAYGSAXDLICT  124

Query  162  HFMDGMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSNLSMI  221
            HFMDGMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISDGKVYLSGLRSNLSMI
Sbjct  125  HFMDGMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISDGKVYLSGLRSNLSMI  184

Query  222  SHGQRQRVVIDPFKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHVPFKD  281
            SHGQRQRVVIDPFKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHVPFKD
Sbjct  185  SHGQRQRVVIDPFKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHVPFKD  244

Query  282  MPATQMLLEKLNGTVFCLLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPS  341
            MPATQMLLEKLNGTVFCLLDTSTIPAEELTMS SRS ANSGLSDSL TTSTPR SNGDSPS
Sbjct  245  MPATQMLLEKLNGTVFCLLDTSTIPAEELTMSSRSANSGLSDSLATSTPRTSNGDSPS  304

Query  342  HPYKRTTSPHFHHFVEQCLQRNPDARPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT  401
            HPYKRTTSPHFHHFVEQCLQRNPD RPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT
Sbjct  305  HPYKRTTSPHFHHFVEQCLQRNPDVRPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT  364

Query  402  NFEGSQSQDHSGIFGLVTNLEELEVDDWEF  431
            NFEGSQ QDHSGIFGLVTNLEELEVDDWEF
Sbjct        NFEGSQ QDHSGIFGLVTNLEELEVDDWEF
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Sbjct  365  NFEGSQPQDHSGIFGLVTNLELEVDDWEF  394


>ref|NP_001015603.1| [UGM] STE20-related kinase protein alpha [Bos taurus]
 ref|NP_001155356.1| [UG] STE20-related kinase adapter protein alpha [Ovis aries]
 sp|Q5R9J9.1|STRAA_BOVIN [G] RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD
 alpha; AltName: Full=STE20-related adapter protein
 gb|AAX08938.1| [G] protein kinase LYK5 isoform 4 [Bos taurus]
 gb|ACR46653.1| [G] STRADA [Ovis aries]
 gb|DAA18360.1| [G] STE20-related kinase adapter protein alpha [Bos taurus]
Length=373

 GENE ID: 515024 STRADA | STE20-related kinase adaptor alpha [Bos taurus]
 (10 or fewer PubMed links)

 Score =  748 bits (1932),  Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 356/373 (96%), Positives = 362/373 (98%), Gaps = 0/373 (0%)

Query  59   MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTFLQGE  118
            MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTFLQGE
Sbjct  1    MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTFLQGE  60

Query  119  LHVSKLFNHPNIVPYRATFIADNELAVVTSFMAYGSAKDLICTHFMDGMSELAIAYILQG  178
            LHVSKLF+HNI+PY ATFIADNELAVVTSFMAYGSAKDLICTHFMDGM+ELAIAYILQG
Sbjct  61   LHVSKLFSHPNILPYGATFIADNELAVVTSFMAYGSAKDLICTHFMDGMSELAIAYILQG  120

Query  179  VLKALDYIHHMGYVHRSVKASHILLSVDGKVYLSGLRSNLSMISHGORQVVHDPKYS+   238
            +LKALDYIHHMGYVHRSVKASH+LIS DGKVYLSGLRSNLSMISHGORQVVHDPKYS+
Sbjct  121  ALKALDYIHHMGYVHRSVKASHVLISADGKVYLSGLRSNLSMISHGOQRQVVHDPKYSI  180

Query  239  KVLPWLSPEVLQONLQGYDAKSDIYSVGITACELANGHVPFKDMPATQMLLEKLNGTVPC  298
            KVLPWL+PEVLQONLQGYDAKSDIYSVGITACELANGHVPFKDMPATQMLLEKLNGTVPC
Sbjct  181  KVLPWLEPEVLQONLQGYDAKSDIYSVGITACELANGHVPFKDMPATQMLLEKLNGTVPC  240

Query  299  LLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPSHPYHRTFSPHFHHFVEQ  358
            LLDTSTIPAEELTMS SRS ANSGLS+SL   STPR SNGDSPSHPYHRTFSPHFHHFVEQ
Sbjct  301  LLDTSTIPAEELTMSTSKSAANSGLSESLAPSTPRTSNGDSPSHPYHRTFSPHFHHFVEQ  300

Query  359  CLQRNPDARPSASTLLNHSFFKQIKRRASEALPELLRPVTPITNFEGSQSQDHSGIFGLV  418
            CLQRNPD PSASTLLNHSFFKQIKRRASEALPELLRPVTPIT PEG QSQDHSGIFGLV
Sbjct  301  CLQRNFDRPSASTLLNHSFFKQIKRRASEALPELLRPVTPITTFEGRQSQDHSGIFGLV  360

Query  419  TNLEELEVDDWEF  431
            TNLEELEVDDWEF
Sbjct  361  TNLENLEVDDWEF  373


>ref|NP_082402.1| [UGM] STE20-related kinase adapter protein alpha [Mus musculus]
 dbj|BAB27626.1| [G] unnamed protein product [Mus musculus]
 gb|AAQ24157.1| [G] protein kinase LYK5 splice variant 1 [Mus musculus]
 gb|AAH58517.1| [G] RIKEN cDNA 2610019A05 gene [Mus musculus]
 gb|ABK42491.1| [G] STLK5 [synthetic construct]
 emb|CAM27017.1| [G] novel protein [Mus musculus]
 gb|EDL34272.1| [G] RIKEN cDNA 2610019A05, isoform CRA_a [Mus musculus]
 gb|EDL34273.1| [G] RIKEN cDNA 2610019A05, isoform CRA_b [Mus musculus]
Length=394

 GENE ID: 72149 Strada | STE20-related kinase adaptor alpha [Mus musculus]
 (Over 10 PubMed links)

 Score =  775 bits (2001),  Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 369/390 (95%), Positives = 380/390 (98%), Gaps = 0/390 (0%)

Query  42   TNDASSESIASFSKQEVMSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRR  101
            N+ASSESIASFSK E+MSSFLPEGGCYELLT-IGKGFEDLMTVNLARYKPTGEYVTVRR
Sbjct  5    ANEASSESIASFSKPEMMMSSFLPEGGCYELLTIIGKGFEDLMTVNLARYKPTGEYVTVRR  64

Query  102  INLEACSNEMVTFLQGELHVSKLFNHPNIVPYRATFIADNELAVVTSFMAYGSAKDLICT  161
            INLEACSNEMVTFLQGELHVSKLF+HNIVPYRATFIADNELAVVTSFMAYGSAKDLI T
Sbjct  65   INLEACSNEMVTFLQGELHVSKLFSHPNIVPYRATFIADNELAVVTSFMAYGSAKDLIGT  124

Query  162  HFMDGMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSNLSMI  221
            HFMDGMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILIS DGKVYLSGLRSNLSMI
Sbjct  125  HFMDGMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILIS TDGKVYLSGLRSNLSMI  184

Query  222  SHGQRQRVVHDPPKYSVKVLPWLSPEVLQONLQGYDAKSDIYSVGITACELANGHVPFKD  281
            SHGQRQR VHDPPKY++VLPWL+PEVLQONLQGYDAKSDIYSVGITACELANGHVPFKD
Sbjct  185  SHGQRQRAVHDPYKYSIKVLPWLEPEVLQONLQGYDAKSDIYSVGITACELANGHVPFKD  244

Query  282  MPATQMLLEKLNGTVPCLLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPS  341
            MPATQMLLEKLNGTVPCLLDTSTIPAEELTMSFSRS+AN GL+DSL   + RPSNGDSPS
Sbjct  245  MPATQMLLEKLNGTVPCLLDTSTIPAEELTMSFSRSIANPGLSDSLAAGSLRPSNGDSPS  304

Query  342  HPYHRTFSPHFHHFVEQCLQRNDARPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT  401
            HPYHRTFSPH+FVEQCLQRNDARP+ASTLLNHSFFKQIKRRASEALPELLRPVTPIT
Sbjct  305  HPYHRTFSPHHFVEQCLQRNDARPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT  364

Query  402  NFEGSQSQDHSGIFGLVTNLELEVDDWEF  431
            NFEGSQSQDHSGIFGLVTNLE+LEVDDWEF
Sbjct  365  NFEGSQSQDHSGIFGLVTNLEDLEVDDWEF  394
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>ref|NP_877972.1| UGM STE20-related kinase adapter protein alpha [Rattus norvegicus]
 sp|Q7TNZ6.1|STRAA_RAT G RecName: Full=STE20-related kinase adapter protein alpha; Short=STRAD
alpha; AltName: Full=STE20-related adapter protein
 gb|AAP92801.1| G protein kinase LYK5 [Rattus norvegicus]
Length=333

 GENE ID: 303605 Strada | STE20-related kinase adaptor alpha [Rattus norvegicus]
(10 or fewer PubMed links)

 Score = 758 bits (1958), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 362/390 (93%), Positives = 377/390 (97%), Gaps = 1/390 (0%)

Query  42   TNDASSESIASFSKQEVMSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGSYVTVRR  101
            N+ASSESIASFSK E+MSSFLPEGGCYELL+VIGKGFEDLMTVN +RYKPTGSYVTVRR
Sbjct  5    ANEASSESIASFSKFEIMSSFLPEGGCYELLSVIGKGFEDLMTVN-SRYKPTGSYVTVRR  63

Query  102  INLEACSNEMVTFLQGELHVSKLFNHPNIVPYRATFIADNELMVVTSFMAYGSAKDLICT  161
            INLEACSNEMVTFLQGELHVSKLF+HPNIVPYRATFIADNELM VTSFMAYGSAKDLI T
Sbjct  64   INLEACSNEMVTFLQGELHVSKLFSHPNIVPYRATFIADNELWAVTSFMAYGSAKDLIGT  123

Query  162  HFMDGMNELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSNLSMI  221
            HFMDGM+ELAIAYILQGVLKALDYIHHMGYVHRSVKASHILIS DGKVYLSGLRSNLSMI
Sbjct  124  HFMDGMSELAIAYILQGVLKALDYIHHMGYVHRSVKASHILISTDGKVYLSGLRSNLSMI  183

Query  222  SHGQRQRVVEDPPKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHVPPKD  281
            SHGQR VEDPPKYS+KVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHVPPKD
Sbjct  184  SHGQRQRAVHDPPKYSIKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHVPPKD  243

Query  282  MPATQMLLEKLNGTVPCLLDTSTIPAEELTMSPSRSVANSGLSDSL/TTSTPRPSNGDSPS  341
            MPATQMLLEKLNGTVPCLLDTSTIPAEELTMSPSRS+AN GL+DSL + RP+NGDSPS
Sbjct  244  MPATQMLLEKLNGTVPCLLDTSTIPAEELTMSPSRSIANPGLHDSLAAGSLRPANGDSPS  303

Query  342  HPYHRTFSPHFHHFVEQCLQRNPDARPSASTLLNHSFFKQIKRRASEALPELLRPVTPIT  401
            HPYHRTFSPHFH+FVEQCLQRNPDARP+ASTLLNHSFFKQIKRRASEALPELLRPVTPIT
Sbjct  304  HPYHRTFSPHFHNFVEQCLQRNPDARPNASTLLNHSFFKQIKRRASEALPELLRPVTPIT  363

Query  402  NFEGSQSQDRSGTFGLVTNLESLEVDDWEF  431
            +FEGSQSQDHSGI GLVTNLE+LEVDDWEF
Sbjct  364  SFEGSQSQDHSGILGLVTNLEDLEVDDWEF  393
```

Select All Get selected sequences Distance tree of results Multiple alignment